

FINAL REPORT NARRATIVE

Full title:

**Pilot Investigation of Large-Scale Biologically Realistic Models of Cortical
Microcircuit Dynamics with Application to Novel Statistical Classifiers**

N00014-99-1-0880

June–December, 1999

Principal investigator:

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FINAL PROGRESS SUMMARY

The purpose of this project was to begin to address a major gap in our conceptual understanding of synaptic and brain-like network dynamics, and with it our present inability to benefit from the potential technological applications of pulse-coding networks. We narrowed the gap by incorporating newly discovered biological parameters (obtained from a co-investigator's work on another ONR-funded project) into large-scale computer simulations of up to 1000 neurons organized into biologically and spatially realistic layers and columns. We achieved the requisite computational speed through the use of parallel distributed processing (analogous to the strategy the brain uses), using an inexpensive "Beowulf" clustering of eight computer processing boards.

The project was initiated 1 June 1999. The first modification was to break out the Matlab core processing loop into a separate program that uses text files for input and output. This enabled Matlab to be used to design and inspect networks before simulation begins, and to later visualize and analyze the results. We were able to perform robustness experiments on an excitatory network of 320 cells, demonstrating a gentle, sigmoidally-shaped decline in recall with cumulative random lesioning of interconnections (synapses). A particular potassium channel seems to be essential to robust synchronous firing.

We then successfully translated the initial version Matlab code (the CPU-intensive processing section) into C language for Windows and LINUX, and tested it on mixed excitatory-inhibitory networks of up to 1000 cells. Using a single processor, the C language code increased processing efficiency 24-fold compared to Matlab. This version 1 code was then rewritten for distributed processing on time borrowed from an existing 20-Pentium II-CPU Beowulf cluster. Initial time trials performed on cortical networks of 2 to 1000 cells suggests that the total time does not depend as heavily on the product (connection probability) x (N cells)squared as projected earlier, but rather shows a substantial linear term:

Interconnection Probability	Simulated N cells	Duration(sec)	Actual Time to Complete (sec)
.01	1000	1000	110.37
.001	1000	1000	107.16
.081	320	1000	22.36

If these projections hold up, a 1-million-cell simulation would take about 5.6 days on a single CPU, or roughly 6 hours on the proposed 30-CPU Beowulf system (assuming that each CPU "manages" a single cortical column. The remainder of the pilot effort was devoted to redesigning the interface to broaden the scope of allowable parameters (based on recently discovered dynamics of inhibitory synapses), plan a move to a C++ rather than C-language implementation, devising learning and testing paradigms for the large-scale simulations, and planning for head-to-head comparison of these brain-like pulse-coded networks with traditional statistical classifiers.

MILESTONES

June 1999: Core processing loop broken out into a separate program that uses text files for input and output.

June 1999: Robustness experiments on an network of 320 excitatory cells demonstrated a gentle, sigmoidally-shaped decline in recall with cumulative random lesioning of interconnections (synapses).

July 1999: Specific potassium channel identified as potentially important to robust synchronous firing.

August 1999: Version 1 Matlab intensive-processing code successfully converted into C language for Windows and LINUX.

September 1999: Initial distributed-processing time trials performed on cortical networks of up to 1000 cells suggests that the total time does not depend as heavily on the product (connection probability) x (N cells)squared as projected earlier, but rather shows a substantial linear term.

December 1999: Completed general design of C++ based simulator that allows dynamic parameter and stimulation specification, compartmental models, no inherent limitation on connectivity or number of simulated neurons.

3a. Significance: What is the scientific, military, and commercial impact of your accomplishments?

Distributed processing of simulated brain-like cellular networks is computationally feasible; early projections demonstrate robust learning and suggest specific ionic channels that may underlie synchronous pulse-coding. Applications may include rapid automated target recognition, military navigation, real-time human gesture recognition, human decision support, and EEG model networks to monitor operator fatigue.

3b. Accomplishment: Highlight your SINGLE most important accomplishment for this reporting period.

Most important accomplishment is the successful conversion of the computationally intensive programming code from vector format to distributed-processing Beowulf C code.

4. Techn Transfer: None

5. Database Stats if desired: None

6. Journal Articles: None

7. Books or Chapters: None

8. TRs: None

9. Conf Papers: None

10. Presentations:

1. Wiezmann Institute of Science lecture colloquium, Oct. 1999
Presented overview of research initiative and progress to audience of biomedical scientists
2. French National Laboratory, Paris, Oct. 1999
Presented overview of research initiative and progress to audience of biomedical scientists
2. American Federation for Medical Research, Jan. 2000
Presented abstract of 300-cell neocortical simulation
3. Office of Naval Research, Feb. 2000
Presented key findings to Program Officer Thomas McKenna

11. Patents: None

12. Honors: None

13. Other Work: None

REPORT DOCUMENTATION PAGE

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14. ABSTRACT The purpose of this project was better understand brain-like network dynamics by incorporated biological parameters into large-scale computer simulations using parallel distributed "Beowulf" clustering. Milestones included improved single-processor efficiency of 24-fold. On multiprocessor clusters, initial time trials on networks of 2 to 1000 cells suggests that the total time does not depend as heavily on the product (connection probability) x (N cells)squared, but shows a substantial linear term. The projected time to ran a 1-million cell simulation would be about 5.6 days on a single CPU, or roughly 6 hours on the proposed 30-CPU Beowulf system. Substantial progress was made toward a C++ implementation for subsequent research.					
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